

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 6, 2004, 19:23:00 ; Search time 112.781 Seconds
(without alignments)
28.627 Million cell updates/sec

Title: US-10-618-644-4

Perfect score: 58

Sequence: 1 IPFGVPPYWT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_23Sep04:*

1: Geneseqp1980s:*

2: Geneseqp1980s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	9	5 ABB81806	Abb81806 Soybean a
2	58	100.0	517	5 ABG71267	Abg71267 Glycine m
3	58	100.0	517	7 ADL90189	Adl90189 Soybean g
4	58	100.0	562	5 ABG71268	Abg71268 Glycine m
5	52	89.7	561	1 AAP61363	Aap61363 Soybean g
6	52	89.7	562	7 ADH89249	Adh89249 G. max gl
7	52	89.7	562	7 ADL90188	Adl90188 Soybean g
8	52	89.7	562	8 ADG43984	Adg43984 G. max gl
9	49	84.5	484	1 AAP71081	Aap71081 Sequence
10	49	84.5	540	2 AAU19632	Aau19632 Human ost
11	48	82.8	516	1 AAP61362	Aap61362 Soybean g
12	48	82.8	516	7 ADH89251	Adh89251 G. max gl
13	48	82.8	516	8 ADG43986	Adg43986 G. max gl
14	43	74.1	334	7 ADH8130	Adh8130 Enterococ
15	42	72.4	8	2 AAR76989	Aar76989 Immune st
16	42	72.4	8	2 AAU07491	Aau07491 Soybean p
17	42	72.4	98	6 ABU07828	Abu07828 Rice ster
18	42	72.4	112	4 AAU86535	Aau86535 Novel hum
19	42	72.4	112	7 ADB59869	Adb59869 Connectiv
20	42	72.4	227	6 ABU07834	Abu07834 Corn ster
21	42	72.4	240	2 AAR15263	Aar15263 Extracell
22	42	72.4	323	4 AAU40380	Aau40380 Human pol
23	42	72.4	323	4 AAB93686	Aab93686 Human pro
24	42	72.4	323	5 AAU78084	Aau78084 Human pho
25	42	72.4	323	8 ADN04862	Adn04862 Antipsori

ALIGNMENTS

RESULT 1

ABB81806

ID ABB81806 standard; peptide; 9 AA.

XX

AC ABB81806;

XX

DT 23-SEP-2002 (first entry)

XX

DE Soybean angiotensin converting enzyme inhibitory peptide #4.

XX

KW Soybean; angiotensin converting enzyme inhibitor; hypertension;

KW hypotensive; taste.

XX

OS Glycine max.

XX

PN WO200255546-A1.

XX

PD 18-JUL-2002.

XX

PF 15-JAN-2002; 2002WO-JP000194.

XX

PR 16-JAN-2001; 2001JP-00007400.

PR

PR 04-OCT-2001; 2001JP-00308974.

XX

PA (AJIN) AJINOMOTO CO INC.

XX

PI Kodera T, Nio N;

XX

DR WPI; 2002-520117/55.

XX

PT Peptides, useful as hypotensive agents or in health foods.

XX

PS Claim 1; Page 19; 43pp; Japanese.

XX

CC The invention relates to a novel set of peptides and their salts. The

CC peptides of the invention have hypotensive activity. The peptides are

CC used as hypotensive agents or in health foods, and have favourable taste.

CC The present sequence represents a peptide of the invention, having

CC angiotensin converting enzyme inhibitory activity

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 58; DB 5; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.7e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IPFGVPPYWT 9

|||||||

Aam42166 Human pol
Aay36913 Protein i
Adi45321 Rice isop
Aay35028 C. pneumo
Aar15266 Clone pTB
Abb66815 Drosophi
Aar15269 Clone pTB
Aad47011 Human pro
Ado26840 Human rec
Aar14280 Murine KG
Aar10933 KGF recep
Aab29284 Protein e
Adp29709 Human sec
Adh80696 Human nov
Aau14378 Human nov
Aau14142 Human nov
Abr62853 Mouse am
Abg98511 Human pro
Aab99558 Amino aci
Aae32068 Human TRI

26 42 72.4 324 4 AAM42166
27 42 72.4 344 2 AAY36913
28 42 72.4 363 8 ADI45321
29 42 72.4 517 2 AAY35028
30 42 72.4 526 2 AAR15266
31 42 72.4 555 4 ABB66815
32 42 72.4 652 2 AAR15269
33 42 72.4 654 7 AAD47011
34 42 72.4 672 8 ADO26840
35 42 72.4 726 2 AAR14280
36 42 72.4 726 2 AAR10933
37 41 70.7 330 6 AAB29284
38 41 70.7 452 8 ADP29709
39 41 70.7 1069 4 ADH80696
40 41 70.7 1070 4 AAU14378
41 41 70.7 1194 4 AAU14142
42 41 70.7 1470 7 ABR62853
43 41 70.7 1499 5 ABG98511
44 41 70.7 1499 6 AAB99558
45 41 70.7 1499 6 AAE32068

```

Db          1 IPPGVPIYWT 9

RESULT 2
ABG71267
ID ABG71267 standard; protein; 517 AA.
XX
AC ABG71267;
XX
DT 17-DEC-2002 (first entry)
XX
DE Glycine max (Soybean) var. Wasesuzunari protein #1.
XX
KW Soybean; Glycinin; atomic coordinate data; processability; soya protein;
KW Wasesuzunari; protein co-ordinate data.
XX
OS Glycine max.
XX
PN JP2002193996-A.
XX
PD 10-JUL-2002.
XX
PF 21-DEC-2000; 2000JP-00405097.
XX
PR 21-DEC-2000; 2000JP-00405097.
XX
PA (KYOU ) UNIV KYOTO.
XX
DR WPI; 2002-685438/74.
DR N-PSDB; ABS55194.
XX
PT Glycinin, beta-conglycinin and proglycinin, their crystal structures,
PT three dimensional coordinates, three dimensional structured and models
PT and their uses.
XX
PS Disclosure; Page 1276-1278; 1298pp; Japanese.
XX
CC The present invention relates to a new Glycinin characterised by the
CC atomic coordinate data fully defined in the specification. The structure
CC can be used for improving processability of soya protein. The present
CC amino acid sequence represents the Glycine max (Soybean) var.
CC Wasesuzunari protein #1, as described in the specification
XX
SQ Sequence 517 AA;
Query Match 100.0%; Score 58; DB 5; Length 517;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IPPGVPIYWT 9
Db 149 IPPGVPIYWT 157

RESULT 3
ADL90189
ID ADL90189 standard; protein; 517 AA.
XX
AC ADL90189;
XX
DT 20-MAY-2004 (first entry)
XX
DE Soybean glycinin G5 protein.
XX
KW immunomodulator; immunotherapy; allergen characterisation;
KW immunoglobulin E; allergen sensitivity; soybean; glycinin G5;
KW acidic protein.
XX
OS Glycine max.
XX
PN US2003166518-A1.
XX
PD 04-SEP-2003.

XX 12-JAN-2001; 2001US-00759967.
XX
XX 13-JAN-2000; 2000US-0175948P.
PR 03-MAR-2000; 2000US-0186724P.
XX
PA (BEAR/) BEARDSLEE T A.
PA (ZEEC/) ZEECE M G.
PA (SARA/) SARATH G.
PA (MARK/) MARKWELL J P.
XX
PI Beardslee TA, Zeece MG, Sarath G, Markwell JP;
XX
XX WPI; 2003-898094/82.
XX
PT Allergen characterization comprises obtaining a recombinant fusion
PT protein and detecting the binding of immunoglobulin E molecules in the
PT biological sample to the recombinant fusion protein.
XX
PS Disclosure; SEQ ID NO 23; 34pp; English.
XX
CC The invention describes a method of allergen characterisation comprising:
CC obtaining a recombinant fusion protein; attaching the recombinant fusion
CC protein to a substrate through the native protein; contacting the
CC recombinant fusion protein attached to the substrate with a biological
CC sample from an individual; and detecting the binding of immunoglobulin E
CC molecules in the biological sample to the recombinant fusion protein.
CC Also described are: a method for determining the sensitivity of an
CC individual to a suspected allergen; a method for determining the amount
CC of immunoglobulin E specific for an allergen in a biological sample; a
CC method of immunotherapy; a method of allergen characterisation; a method
CC for determining the sensitivity of an individual to a suspected allergen;
CC a method of determining the amount of immunoglobulin E specific for an
CC allergen in a biological sample; a kit comprising the recombinant fusion
CC protein and instructions for using the recombinant fusion protein to
CC determine IgE binding to the know or suspected allergen; and a method for
CC epitope determination. The method is useful for characterising allergens.
CC This is the amino acid sequence of soybean glycinin G2 acidic protein
CC that can be used to demonstrate the methods of the invention.
XX
SQ Sequence 517 AA;
Query Match 100.0%; Score 58; DB 7; Length 517;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IPPGVPIYWT 9
Db 149 IPPGVPIYWT 157

RESULT 4
ABG71268
ID ABG71268 standard; protein; 562 AA.
XX
AC ABG71268;
XX
DT 17-DEC-2002 (first entry)
XX
DE Glycine max (Soybean) cv. Forrest protein.
XX
KW Soybean; Glycinin; atomic coordinate data; processability; soya protein;
KW Forrest; protein co-ordinate data.
XX
OS Glycine max.
XX
PN JP2002193996-A.
XX
PD 10-JUL-2002.
XX
PF 21-DEC-2000; 2000JP-00405097.
XX
PR 21-DEC-2000; 2000JP-00405097.
PR

```

XX PA (KYOU) UNIV KYOTO.
 XX DR WPI; 2002-695438/74.
 XX DR N-PSDB; ABS55195.
 XX PT Glycinin, beta-conglycinin and proglycinin, their crystal structures,
 XX PT three dimensional coordinates, three dimensional structured and models
 XX PT and their uses.
 XX PS Disclosure; Page 1280-1282; 1298pp; Japanese.
 XX CC The present invention relates to a new Glycinin characterised by the
 XX CC atomic coordinate data fully defined in the specification. The structure
 XX CC can be used for improving processability of soya protein. The present
 XX CC amino acid sequence represents the Glycine max (soybean) cv. Forrest
 XX CC protein, as described in the specification
 XX SQ Sequence 562 AA;
 Query Match 100.0%; Score 58; DB 5; Length 562;
 Best Local Similarity 100.0%; Pred. No. 4.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IPPGVPIWT 9
 DB 148 IPPGVPIWT 156
 RESULT 5
 AAP61363
 ID AAP61363 standard; protein; 561 AA.
 AC AAP61363;
 XX 25-MAR-2003 (revised)
 DT 16-OCT-1991 (first entry)
 XX XX
 XX Soybean glycinin ASA4B3 subunit.
 DE Soybean protein; glycinin.
 KW Glycine max.
 OS JP61132189-A.
 PN 19-JUN-1986.
 XX 03-DEC-1984; 84JP-00254217.
 XX 03-DEC-1984; 84JP-00254217.
 XX (NORQ) NORINSHO KK.
 XX WPI; 1986-200545/31.
 DR N-PSDB; AAN60940.
 XX Prepn. of soybean messenger RNA - for insertion into cells or
 PT microorganisms to produce soybean protein.
 XX Example 2; Fig 2; 7pp; Japanese.
 XX Sequence derived from mRNA may be used for the expression of the soybean
 CC protein by a foreign host. (Updated on 25-MAR-2003 to correct PA field.)
 XX SQ Sequence 561 AA;
 Query Match 89.7%; Score 52; DB 1; Length 561;
 Best Local Similarity 88.9%; Pred. No. 30;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 IPPGVPIWT 9
 ||| |||||

DB 148 IPPSVPIWT 156
 RESULT 6
 ADH89249
 ID ADH89249 standard; protein; 562 AA.
 XX AC ADH89249;
 XX DT 06-MAY-2004 (first entry)
 XX XX
 XX DE G. max glycinin ASA4B3 subunit.
 XX KW double stranded RNA; storage protein; 2S-albumen; 7S-globulin;
 KW 11S/12S-globulin; zein-prolamine; homogentisate metabolic pathway;
 KW pharmaceutical; plant; abiotic stress; fatty acid composition;
 KW lipid composition; oil composition; carbohydrate composition; colour;
 KW pigmentation; pathogen resistance; fruit ripening delay; aging;
 KW male sterility; lignin; fibre; cotton; Vitamin E synthesis; nicotine;
 KW caffeine; theophylline; threonine biosynthesis; glycinin.
 XX OS Glycine max.
 XX PN WO2003078629-A1.
 XX XX
 XX PD 25-SEP-2003.
 XX PF 17-MAR-2003; 2003WO-BP002735.
 XX PR 20-MAR-2002; 2002DE-01012892.
 XX PA (BADI) BASF PLANT SCI GMBH.
 XX PI Kock M, Bauer J;
 XX WPI; 2003-803889/75.
 DR N-PSDB; ADH89248.
 XX Reducing expression of at least two target genes, useful e.g. for
 PT producing transgenic plants, using partly double-stranded interfering
 PT RNA.
 XX Disclosure; SEQ ID NO 24; 228pp; German.
 CC This invention describes a novel method for reducing the expression of at
 CC least two different endogenous target genes in a eukaryotic cell or
 CC organism by introducing an RNA molecule that is at least partly double
 CC stranded. The transcribed RNAs from at least two target genes have
 CC homology below 90% and the RNA molecule is formed as a single, self-
 CC complementary molecule. At least one of the double-stranded structures
 CC formed from individual sense sequences has an even number of repeats of
 CC 21 or 22 bp. The RNA molecule may include an intron-encoding sequence. At
 CC least two target genes are selected from different classes of storage
 CC protein genes, i.e. 2S-albumen, 7S- or 11S/12S-globulins or zein-
 CC prolamine and at least one of the sense sequences is identical to storage
 CC protein sequences or genes in the homogentisate metabolic pathway or
 CC enzyme types, e.g. acetyl transacylases, thioesterases, (de)branching
 CC expression systems, vectors and transgenic organisms are used for
 CC preparation of pharmaceuticals, in biotechnological processes and plant
 CC biotechnology, specifically in plants to improve protection against
 CC abiotic stress, to modify composition and/or content of fatty acids,
 CC lipids and oils, to modify carbohydrate composition, to alter colour or
 CC pigmentation, to reduce content of storage proteins, to increase
 CC resistance to pathogens, to inhibit stem break, to delay fruit ripening
 CC or aging, to induce male sterility, to reduce content of toxic or
 CC unwanted components, to modify lignification and/or lignin content, to
 CC modify the fibre component in foods or fibre quality in cotton, to reduce
 CC susceptibility to shock, to increase synthesis of Vitamin E, to reduce
 CC contents of nicotine, caffeine or theophylline and to increase methionine
 CC content, by reducing threonine biosynthesis. The method provides a rapid
 CC and efficient way of reducing gene expression, can inhibit more than one
 CC target gene, prevents development of multiple phenotypes (since the

CC transcription rate is the same for all RNA sequences, significantly
 CC reducing the selection process required to produce an organism with
 CC effective suppression of all target genes), avoids problems of epigenetic
 CC gene silencing, does not require synthesis of individual RNA sequences
 CC and the method can be applied to plants with complex (polyploid) genomes.
 CC No interference between the individual RNA sequences occur. This sequence
 CC represents a protein encoded by a target gene used in the method of the
 CC invention.

XX Sequence 562 AA;

Query Match 89.7%; Score 52; DB 7; Length 562;
 Best Local Similarity 88.9%; Pred. No. 31;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IPPGVVYWT 9
 DB 149 IPPSVFYWT 157

RESULT 7
 ADL90188
 ID ADL90188 standard; protein; 562 AA.
 XX
 AC ADL90188;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Soybean glycinin G4 protein.
 XX
 DE immunomodulator; immunotherapy; allergen characterisation;
 KW immunoglobulin E; allergen sensitivity; soybean; glycinin G4;
 KW acidic protein.
 XX
 OS Glycine max.
 XX
 PN US2003166518-A1.
 XX
 PD 04-SEP-2003.
 XX
 PF 12-JAN-2001; 2001US-00759967.
 XX
 PF 13-JAN-2000; 2000US-0175948P.
 PR 03-MAR-2000; 2000US-0186724P.
 XX
 PR (BEAR/) BEARDSLEE T A.
 PA (ZEEC/) ZEECE M G.
 PA (SARA/) SARATH G.
 PA (MARK/) MARKWELL J P.
 XX
 XX Beardslee TA, Zeece MG, Sarath G, Markwell JP;
 FI WPI; 2003-898094/82.
 XX
 DR Allergen characterization comprises obtaining a recombinant fusion
 PT protein and detecting the binding of immunoglobulin E molecules in the
 PT biological sample to the recombinant fusion protein.
 XX
 PS Disclosure; SEQ ID NO 22; 34pp; English.

CC The invention describes a method of allergen characterisation comprising:
 CC obtaining a recombinant fusion protein; attaching the recombinant fusion
 CC protein to a substrate through the native protein; contacting the
 CC recombinant fusion protein attached to the substrate with a biological
 CC sample from an individual; and detecting the binding of immunoglobulin E
 CC molecules in the biological sample to the recombinant fusion protein.
 CC Also described are: a method for determining the sensitivity of an
 CC individual to a suspected allergen; a method for determining the amount
 CC of immunoglobulin E specific for an allergen in a biological sample; a
 CC method of immunotherapy; a method of allergen characterisation; a method
 CC for determining the sensitivity of an individual to a suspected allergen;
 CC a method of determining the amount of immunoglobulin E specific for an
 CC allergen in a biological sample; a kit comprising the recombinant fusion

CC protein and instructions for using the recombinant fusion protein to
 CC determine IgE binding to the known or suspected allergen; and a method for
 CC epitope determination. The method is useful for characterising allergens.
 CC This is the amino acid sequence of soybean glycinin G2 acidic protein
 CC that can be used to demonstrate the methods of the invention.

XX Sequence 562 AA;

Query Match 89.7%; Score 52; DB 7; Length 562;
 Best Local Similarity 88.9%; Pred. No. 31;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IPPGVVYWT 9
 DB 149 IPPSVFYWT 157

RESULT 8
 ADG43984
 ID ADG43984 standard; protein; 562 AA.
 XX
 AC ADG43984;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE G. max glycinin A5A4B3 subunit protein.
 XX
 DE oil content; plant; storage protein; seed-specific promoter; 2S-albumin;
 KW 7S-globulin; 11S-globulin; 12S-globulin; zein-prolamine; transgenic;
 KW oil production; fat production; free fatty acid production; food;
 KW animal feed; pharmaceutical; fine chemical production; glycinin.
 XX
 OS Glycine max.
 XX
 PN WO200307643-A2.
 XX
 PD 25-SEP-2003.
 XX
 PF 17-MAR-2003; 2003WO-EP002733.
 XX
 PR 20-MAR-2002; 2002DE-01012893.
 XX
 PA (BADI) BASF PLANT SCI GMBH.
 XX
 PI Bauer J;
 XX
 XX WPI; 2004-011485/01.
 DR N-PSDB; ADG43983.
 XX
 PT Increasing total oil content of plants, useful e.g. as foods or animal
 PT feeds, by reducing amount of storage proteins, particularly with double-
 PT stranded interfering RNA.
 XX
 PS Claim 4; SEQ ID NO 24; 253pp; German.

CC This invention describes a novel method for increasing the total oil
 CC content of a plant by reducing the amount of at least one storage protein
 CC in the plant (or its tissue, organs, parts or cells) and selecting plants
 CC that have higher total oil content than starting plants. The storage
 CC protein is suppressed by introducing antisense RNA, optionally combined
 CC with a ribozyme, sense RNA that induces co-suppression, DNA-binding
 CC factors directed against storage protein genes, viral sequences that
 CC degrade storage protein RNA, constructs that induce homologous
 CC recombination of endogenous storage protein genes or mutations into
 CC storage protein genes. Most preferably a plant cell is stably transfected
 CC with a recombinant expression construct, then regenerated to plants that
 CC express the incorporated sequence. The expression constructs particularly
 CC contain a seed-specific promoter and they are introduced into plants by
 CC standard methods, e.g. via Agrobacterium. The preferred storage proteins
 CC of the invention are 2S-albumens, 7S or 11S/12S-globulins or zein-
 CC prolamines. Transgenic organisms produced by the new method are used for
 CC production of oils, fats, free fatty acids or their derivatives, useful
 CC as foods, animal feeds, pharmaceuticals and fine chemicals. This sequence

CC represents a storage protein used to illustrate the method of the
 CC invention.

XX Sequence 562 AA;

Query Match 89.7%; Score 52; DB 8; Length 562;
 Best Local Similarity 88.9%; Pred. No. 31;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 IPPGVPTWT 9
 |||||
 Db 149 IPPSVPTWT 157

RESULT 9

AAP71081
 ID AAP71081 standard; protein; 484 AA.

XX AC AAP71081;

XX 25-MAR-2003 (revised)

DT 17-APR-1991 (first entry)

XX Sequence encoded by Vicia fabia type B gene.

XX Plant seed protein; nutrition.

XX Vicia fabia.

XX DD240911-A.

XX 19-NOV-1986.

XX 31-DEC-1983; 83DD-00259075.

XX 31-DEC-1983; 83DD-00259075.

XX (DEAK) AKAD WISSENSCHAFTEN DDR.

XX Muntz K, Baesuner R, Saalbach G, Jung R, Wobus U, Weschke W;
 PI Baumlein H;

XX WPI; 1987-080534/12.

XX N-PSDB; AAN71250.

XX Prodn. of plant seed protein genes - by incorporation of codon(s) for
 PT relevant limiting amino acids, e.g. for methionine in leguminous protein
 PT legumin.

XX Example; pp6-9; 12pp; German.

XX The patent claims a method for the prodn. of nutrition- physiologically
 CC improved plant-seed proteins. Suitable plant seed protein genes are the
 CC genes for legumin or vicilin from field beans, or corresponding suitable
 CC genes for seed proteins of cereals. (Updated on 25-MAR-2003 to correct PA
 CC field.)

XX Sequence 484 AA;

Query Match 84.5%; Score 49; DB 1; Length 484;
 Best Local Similarity 77.8%; Pred. No. 70;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 IPPGVPTWT 9

Db 147 IPPSVPTWT 155

RESULT 10

AAW19632

ID AAW19632 standard; protein; 540 AA.

XX AC AAW19632;

XX

DT 01-SEP-1997 (first entry)

XX Human osteo antiviral protein.

XX Osteo antiviral protein; OAP; virucide; picornavirus;

KW necrotising pancreatitis; parotitis; bone injury; osteoporosis;

KW osteodystrophy; osteohypertrophy; osteoma; osteopetrusis; osteoblastoma;

KW therapy; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..19
 FT /label= sig_peptide

XX WO9722623-A1.

XX 26-JUN-1997.

XX 19-DEC-1995; 95WO-US017107.

XX 19-DEC-1995; 95WO-US017107.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ni J, Feng P, Dillon PJ, Gentz R;

XX WPI; 1997-341629/31.

XX N-PSDB; AAT68722.

XX DNA encoding osteo antiviral protein - useful as an antiviral agent,
 PT especially to treat necrotising pancreatitis caused by picornavirus.

XX Claim 1; Fig 1; 63pp; English.

XX A novel human antiviral protein (AAW19632) is designated osteo antiviral
 CC protein (OAP). Its amino acid sequence was deduced from a human tumour
 CC pancreas cDNA clone (AAT68722). OAP is structurally related to Ecml,
 CC showing 66.8% identity to murine Ecml. OAP, esp, the mature protein, can
 CC be expressed in prokaryotic or eukaryotic host cells. It can be used as
 CC an antiviral agent, esp. to treat necrotising pancreatitis and parotitis
 CC caused by picornavirus. It may also be used to promote the healing of
 CC bone fractures, for de novo bone formation and for the treatment of
 CC osteoporosis, as well as for screening for OAP (ant)agonists useful in
 CC the treatment of osteodystrophy, osteohypertrophy, osteoma,
 CC osteopetrusis, osteoporosis and osteoblastoma

XX Sequence 540 AA;

Query Match 84.5%; Score 49; DB 2; Length 540;

Best Local Similarity 87.5%; Pred. No. 78;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 PPGVPYWT 9

Db 300 PPGVPYWT 307

RESULT 11

AAW19632

ID AAP61362 standard; protein; 516 AA.

XX AAP61362;

XX 25-MAR-2003 (revised)

DT 16-OCT-1991 (first entry)

XX Soybean glycinin A3B4 subunit.

XX Soybean protein; glycinin.

XX Glycine max.

Sun Nov 7 14:54:03 2004

```

XX JP61132189-A.
XX
XX 19-JUN-1986.
XX
XX 03-DEC-1984; 84JP-00254217.
XX
XX 03-DEC-1984; 84JP-00254217.
XX
XX (NORQ ) NORINSHO KK.
XX
XX WPI; 1986-200545/31.
XX
XX N-PSDB; AAM60939.
XX
XX Prepn. of soybean messenger RNA - for insertion into cells or
XX microorganisms to produce soybean protein.
XX
XX Example 1; Fig 1; 7pp; Japanese.
XX
XX Sequence derived from mRNA may be used for the expression of the soybean
XX protein by a foreign host. (Updated on 25-MAR-2003 to correct PA field.)
XX
XX Sequence 516 AA;
XX
XX Query Match 82.8%; Score 48; DB 1; Length 516;
XX Best Local Similarity 88.9%; Pred. No. 1e+02;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 IPFGVPYWT 9
XX || |||||
XX Db 149 IPLGVYWT 157
XX
XX RESULT 12
XX ADH89251
XX ID ADH89251 standard; protein; 516 AA.
XX
XX AC ADH89251;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE G. max glycinin A3-B4 subunit.
XX
XX KW double stranded RNA; storage protein; 2S-albumen; 7S-globulin;
XX 11S/12S-globulin; zein-prolamine; homogenistate metabolic pathway;
XX pharmaceutical; plant; abiotic stress; fatty acid composition;
XX lipid composition; oil composition; carbohydrate composition; colour;
XX pigmentation; pathogen resistance; fruit ripening delay; aging;
XX male sterility; lignin; fibre; cotton; Vitamin E synthesis; nicotine;
XX caffeine; theophylline; threonine biosynthesis; glycinin.
XX
XX OS Glycine max.
XX
XX XX WO2003078629-A1.
XX
XX PD 25-SEP-2003.
XX
XX XX 17-MAR-2003; 2003WO-EP002735.
XX
XX PF 20-MAR-2002; 2002DE-01012892.
XX
XX PR (BADI ) BASF PLANT SCI GMBH.
XX
XX XX Kock M, Bauer J;
XX
XX XX WPI; 2003-803889/75.
XX
XX DR N-PSDB; ADH89250.
XX
XX XX Reducing expression of at least two target genes, useful e.g. for
XX PT producing transgenic plants, using partly double-stranded interfering
XX PT RNA.
XX
XX XX Disclosure; SEQ ID NO 26; 228pp; German.
XX
XX

```

```

XX This invention describes a novel method for reducing the expression of at
XX least two different endogenous target genes in a eukaryotic cell or
XX organism by introducing an RNA molecule that is at least partly double
XX stranded. The transcribed RNAs from at least two target genes have
XX homology below 90% and the RNA molecule is formed as a single, self-
XX complementary molecule. At least one of the double-stranded structures of
XX formed from individual sense sequences has an even number of repeats of
XX 21 or 22 bp. The RNA molecule may include an intron-encoding sequence. At
XX least two target genes are selected from different classes of storage
XX protein genes, i.e. 2S-albumen, 7S- or 11S/12S-globulins or zein-
XX prolamine and at least one of the sense sequences is identical to storage
XX protein sequences or genes in the homogenistate metabolic pathway or
XX enzyme types, e.g. acetyl transacylases, thioesterases, (de)branching
XX enzymes or cellulases. The RNA of the invention, also related cassettes,
XX expression systems, vectors and transgenic organisms are used for
XX preparation of pharmaceuticals, in biotechnological processes and plant
XX biotechnology, specifically in plants to improve protection against
XX abiotic stress, to modify carbohydrate composition, to alter colour or
XX lipid and oils, to modify storage proteins, to increase
XX pigmentation, to reduce content of storage proteins, to delay fruit ripening
XX or aging, to induce male sterility, to reduce content of toxic or
XX unwanted components, to modify lignification and/or lignin content, to
XX modify the fibre component in foods or fibre quality in cotton, to reduce
XX susceptibility to shock, to increase synthesis of Vitamin E, to reduce
XX contents of nicotine, caffeine or theophylline and to increase methionine
XX content, by reducing threonine biosynthesis. The method provides a rapid
XX and efficient way of reducing gene expression, can inhibit more than one
XX target gene, prevents development of multiple phenotypes (since the
XX transcribing rate is the same for all RNA sequences, significantly
XX reducing the selection process required to produce an organism with
XX effective suppression of all target genes), avoids problems of epigenic
XX gene silencing, does not require synthesis of individual RNA sequences
XX and the method can be applied to plants with complex (polyploid) genomes.
XX No interference between the individual RNA sequences occur. This sequence
XX represents a protein encoded by a target gene used in the method of the
XX invention.
XX
XX SQ Sequence 516 AA;
XX
XX Query Match 82.8%; Score 48; DB 7; Length 516;
XX Best Local Similarity 88.9%; Pred. No. 1e+02;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 IPFGVPYWT 9
XX || |||||
XX Db 149 IPLGVYWT 157
XX
XX RESULT 13
XX ADG43986
XX ID ADG43986 standard; protein; 516 AA.
XX
XX AC ADG43986;
XX
XX DT 26-FEB-2004 (first entry)
XX
XX XX G. max glycinin A3-B4 subunit protein.
XX
XX DE oil content; plant; storage protein; seed-specific promoter; 2S-albumin;
XX KW 7S-globulin; 11S-globulin; 12S-globulin; zein-prolamine; transgenic;
XX KW oil production; fat production; free fatty acid production; food;
XX KW animal feed; pharmaceutical; fine chemical production; glycinin.
XX
XX OS Glycine max.
XX
XX XX WO2003077643-A2.
XX
XX PD 25-SEP-2003.
XX
XX PF 17-MAR-2003; 2003WO-EP002733.
XX
XX

```


Sun Nov 7 14:54:03 2004

Query Match 72.4%; Score 42; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IPPGVFY 7
Db 2 IPPGVFY 8

Search completed: November 6, 2004, 19:45:48
Job time : 120.781 secs

THIS PAGE BLANK (USPTO)